

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Adair, John R.
Athwal, Diljeet S.
Emtage, John S.
- (ii) TITLE OF INVENTION: Humanised Antibodies
- (iii) NUMBER OF SEQUENCES: 28
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
 - (B) STREET: One Liberty Place - 46th Floor
 - (C) CITY: Philadelphia
 - (D) STATE: PA
 - (E) COUNTRY: USA
 - (F) ZIP: 19103
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/743,329
 - (B) FILING DATE: 17-SEP-1991
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hohenschutz, Liza D.
 - (B) REGISTRATION NUMBER: 33,712
 - (C) REFERENCE/DOCKET NUMBER: CARP-0009
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (215) 568-3100
 - (B) TELEFAX: (215) 568-3439

(2) INFORMATION FOR SEQ ID NO:1:

- ~~(i)~~ SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCCAGATGTT AACTGCTCAC

20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAGGGGCCAG TGGATGGATA GAC

23

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Glu Ile Asn Arg Thr Val Ala Ala
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 18..722

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 84..722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCCAA AGACAAA ATG GAT TTT CAA GTG CAG ATT TTC AGC TTC CTG	50
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu	
-22 -20 -15	
CTA ATC AGT GCC TCA GTC ATA ATA TCC AGA GGA CAA ATT GTT CTC ACC	98
Leu Ile Ser Ala Ser Val Ile Ile Ser Arg Gly Gln Ile Val Leu Thr	
-10 -5 1 5	
CAG TCT CCA GCA ATC ATG TCT GCA TCT CCA GGG GAG AAG GTC ACC ATG	146
Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met	
10 15 20	
ACC TGC AGT GCC AGC TCA AGT GTA AGT TAC ATG AAC TGG TAC CAG CAG	194
Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln	
25 30 35	
AAG TCA GGC ACC TCC CCC AAA AGA TGG ATT TAT GAC ACA TCC AAA CTG	242
Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu	
40 45 50	
GCT TCT GGA GTC CCT GCT CAC TTC AGG GGC AGT GGG TCT GGG ACC TCT	290
Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser	
55 60 65	
TAC TCT CTC ACA ATC AGC GGC ATG GAG GCT GAA GAT GCT GCC ACT TAT	338
Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr	
70 75 80 85	
TAC TGC CAG CAG TGG AGT AGT AAC CCA TTC ACG TTC GGC TCG GGG ACA	386
Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr	
90 95 100	
AAG TTG GAA ATA AAC CGG GCT GAT ACT GCA CCA ACT GTA TCC ATC TTC	434
Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Val Ser Ile Phe	
105 110 115	
CCA CCA TCC AGT GAG CAG TTA ACA TCT GGA GGT GCC TCA GTC GTG TGC	482
Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys	
120 125 130	
TTC TTG AAC AAC TTC TAC CCC AAA GAC ATC AAT GTC AAG TGG AAG ATT	530
Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile	
135 140 145	
GAT GGC AGT GAA CGA CAA AAT GGC GTC CTG AAC AGT TGG ACT GAT CAG	578
Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln	
150 155 160 165	
GAC AGC AAA GAC AGC ACC TAC AGC ATG AGC AGC ACC CTC ACG TTG ACC	626
Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr	
170 175 180	

AAG GAC GAG TAT GAA CGA CAT AAC AGC TAT ACC TGT GAG GCC ACT CAC	674
Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His	
185 190 195	
AAG ACA TCA ACT TCA CCC ATT GTC AAG AGC TTC AAC AGG AAT GAG TGT	722
Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys	
200 205 210	
TAGAGACAAA GGTCCTGAGA CGCCACCACC AGCTCCCAGC TCCATCCTAT CTTCCCTTCT	782
AAGGTCTTGG AGGCTTCCCC ACAAGCGCTT ACCACTGTTG CGGTGCTCTA AACCTCCTCC	842
CACCTCCTTC TCCTCCTCCT CCCTTTCCTT GGCTTTTATC ATGCTAATAT TTGCAGAAAA	902
TATTCAATAA AGTGAGTCTT TGCCTTGAAA AAAAAAAAAA A	943

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser	
-22 -20 -15 -10	
Val Ile Ile Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile	
-5 1 5 10	
Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser	
15 20 25	
Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser	
30 35 40	
Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro	
45 50 55	
Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile	
60 65 70	
Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp	
75 80 85 90	
Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn	
95 100 105	
Arg Ala Asp Thr Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu	
110 115 120	

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
 125 130 135

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
 140 145 150

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
 155 160 165 170

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
 175 180 185

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
 190 195 200

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 205 210

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 41..1444

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 98..1444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCCCCT CTCCACAGAC ACTGAAACT CTGACTCAAC ATG GAA AGG CAC TGG	55
Met Glu Arg His Trp	
-19 -15	
ATC TTT CTA CTC CTG TTG TCA GTA ACT GCA GGT GTC CAC TCC CAG GTC	103
Ile Phe Leu Leu Leu Leu Ser Val Thr Ala Gly Val His Ser Gln Val	
-10 -5 1	
CAG CTG CAG CAG TCT GGG GCT GAA CTG GCA AGA CCT GGG GCC TCA GTG	151
Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val	
5 10 15	
AAG ATG TCC TGC AAG GCT TCT GGC TAC ACC TTT ACT AGG TAC ACG ATG	199
Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met	
20 25 30	

CAC	TGG	GTA	AAA	CAG	AGG	CCT	GGA	CAG	GGT	CTG	GAA	TGG	ATT	GGA	TAC	247
His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	
35					40					45					50	
ATT	AAT	CCT	AGC	CGT	GGT	TAT	ACT	AAT	TAC	AAT	CAG	AAG	TTC	AAG	GAC	295
Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	
				55					60					65		
AAG	GCC	ACA	TTG	ACT	ACA	GAC	AAA	TCC	TCC	AGC	ACA	GCC	TAC	ATG	CAA	343
Lys	Ala	Thr	Leu	Thr	Thr	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	
			70					75					80			
CTG	AGC	AGC	CTG	ACA	TCT	GAG	GAC	TCT	GCA	GTC	TAT	TAC	TGT	GCA	AGA	391
Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	
		85					90					95				
TAT	TAT	GAT	GAT	CAT	TAC	TGC	CTT	GAC	TAC	TGG	GGC	CAA	GGC	ACC	ACT	439
Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	
100						105					110					
CTC	ACA	GTC	TCC	TCA	GCC	AAA	ACA	ACA	GCC	CCA	TCG	GTC	TAT	CCA	CTG	487
Leu	Thr	Val	Ser	Ser	Ala	Lys	Thr	Thr	Ala	Pro	Ser	Val	Tyr	Pro	Leu	
115					120				125						130	
GCC	CCT	GTG	TGT	GGA	GAT	ACA	ACT	GGC	TCC	TCG	GTG	ACT	CTA	GGA	TGC	535
Ala	Pro	Val	Cys	Gly	Asp	Thr	Thr	Gly	Ser	Ser	Val	Thr	Leu	Gly	Cys	
				135					140					145		
CTG	GTC	AAG	GGT	TAT	TTC	CCT	GAG	CCA	GTG	ACC	TTG	ACC	TGG	AAC	TCT	583
Leu	Val	Lys	Gly	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Leu	Thr	Trp	Asn	Ser	
			150					155					160			
GGA	TCC	CTG	TCC	AGT	GGT	GTG	CAC	ACC	TTC	CCA	GCT	GTC	CTG	CAG	TCT	631
Gly	Ser	Leu	Ser	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	
		165					170					175				
GAC	CTC	TAC	ACC	CTC	AGC	AGC	TCA	GTG	ACT	GTA	ACC	TCG	AGC	ACC	TGG	679
Asp	Leu	Tyr	Thr	Leu	Ser	Ser	Ser	Val	Thr	Val	Thr	Ser	Ser	Thr	Trp	
180						185					190					
CCC	AGC	CAG	TCC	ATC	ACC	TGC	AAT	GTG	GCC	CAC	CCG	GCA	AGC	AGC	ACC	727
Pro	Ser	Gln	Ser	Ile	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Ser	Ser	Thr	
195					200					205					210	
AAG	GTG	GAC	AAG	AAA	ATT	GAG	CCC	AGA	GGG	CCC	ACA	ATC	AAG	CCC	TGT	775
Lys	Val	Asp	Lys	Lys	Ile	Glu	Pro	Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys	
				215					220					225		
CCT	CCA	TGC	AAA	TGC	CCA	GCA	CCT	AAC	CTC	TTG	GGT	GGA	CCA	TCC	GTC	823
Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val	
			230					235					240			
TTC	ATC	TTC	CCT	CCA	AAG	ATC	AAG	GAT	GTA	CTC	ATG	ATC	TCC	CTG	AGC	871
Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile	Ser	Leu	Ser	
		245					250					255				

CCC Pro	ATA Ile	GTC Val	ACA Thr	TGT Cys	GTG Val	GTG Val	GAT Val	GTG Val	AGC Ser	GAG Glu	GAT Asp	GAC Asp	CCA Pro	GAT Asp	919	
260 265 270																
GTC Val	CAG Gln	ATC Ile	AGC Ser	TGG Trp	TTT Phe	GTG Val	AAC Asn	AAC Asn	GTG Val	GAA Glu	GTA Val	CAC His	ACA Thr	GCT Ala	CAG Gln	967
275 280 285 290																
ACA Thr	CAA Gln	ACC Thr	CAT His	AGA Arg	GAG Glu	GAT Asp	TAC Tyr	AAC Asn	AGT Ser	ACT Thr	CTC Leu	CGG Arg	GTG Val	GTC Val	AGT Ser	1015
295 300 305																
GCC Ala	CTC Leu	CCC Pro	ATC Ile	CAG Gln	CAC His	CAG Gln	GAC Asp	TGG Trp	ATG Met	AGT Ser	GGC Gly	AAG Lys	GAG Glu	TTC Phe	AAA Lys	1063
310 315 320																
TGC Cys	AAG Lys	GTC Val	AAC Asn	AAC Asn	AAA Lys	GAC Asp	CTC Leu	CCA Pro	GCG Ala	CCC Pro	ATC Ile	GAG Glu	AGA Arg	ACC Thr	ATC Ile	1111
325 330 335																
TCA Ser	AAA Lys	CCC Pro	AAA Lys	GGG Gly	TCA Ser	GTA Val	AGA Arg	GCT Ala	CCA Pro	CAG Gln	GTA Val	TAT Tyr	GTC Val	TTG Leu	CCT Pro	1159
340 345 350																
CCA Pro	CCA Pro	GAA Glu	GAA Glu	GAG Glu	ATG Met	ACT Thr	AAG Lys	AAA Lys	CAG Gln	GTC Val	ACT Thr	CTG Leu	ACC Thr	TGC Cys	ATG Met	1207
355 360 365 370																
GTC Val	ACA Thr	GAC Asp	TTC Phe	ATG Met	CCT Pro	GAA Glu	GAC Asp	ATT Ile	TAC Tyr	GTG Val	GAG Glu	TGG Trp	ACC Thr	AAC Asn	AAC Asn	1255
375 380 385																
GGG Gly	AAA Lys	ACA Thr	GAG Glu	CTA Leu	AAC Asn	TAC Tyr	AAG Lys	AAC Asn	ACT Thr	GAA Glu	CCA Pro	GTC Val	CTG Leu	GAC Asp	TCT Ser	1303
390 395 400																
GAT Asp	GGT Gly	TCT Ser	TAC Tyr	TTC Phe	ATG Met	TAC Tyr	AGC Ser	AAG Lys	CTG Leu	AGA Arg	GTG Val	GAA Glu	AAG Lys	AAG Lys	AAC Asn	1351
405 410 415																
TGG Trp	GTG Val	GAA Glu	AGA Arg	AAT Asn	AGC Ser	TAC Tyr	TCC Ser	TGT Cys	TCA Ser	GTG Val	GTC Val	CAC His	GAG Glu	GGT Gly	CTG Leu	1399
420 425 430																
CAC His	AAT Asn	CAC His	CAC His	ACG Thr	ACT Thr	AAG Lys	AGC Ser	TTC Phe	TCC Ser	CGG Arg	ACT Thr	CCG Pro	GGT Gly	AAA Lys		1444
435 440 445																
TGAGCTCAGC ACCCACAAAA CTCTCAGGTC CAAAGAGACA CCCACACTCA TCTCCATGCT																
TCCCTTGTAT AAATAAAGCA CCCAGCAATG CCTGGGACCA TGTAACAAAAA AAAAAAAAAG																
GAATTC																
1504 1564 1570																

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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Met Glu Arg His Trp Ile Phe Leu Leu Leu Leu Ser Val Thr Ala Gly
-19          -15          -10          -5

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg
      1              5              10

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
    15          20          25

Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    30          35          40          45

Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn
      50          55          60

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser
      65          70          75

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
    80          85          90

Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp
    95          100          105

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Ala Pro
   110          115          120          125

Ser Val Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser
      130          135          140

Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr
      145          150          155

Leu Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro
    160          165          170

Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val
    175          180          185

Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His
   190          195          200          205

Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro
      210          215          220

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Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu
 225 230 235
 Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu
 240 245 250
 Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser
 255 260 265
 Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu
 270 275 280 285
 Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr
 290 295 300
 Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser
 305 310 315
 Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro
 320 325 330
 Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln
 335 340 345
 Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val
 350 355 360 365
 Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val
 370 375 380
 Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu
 385 390 395
 Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg
 400 405 410
 Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val
 415 420 425
 Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg
 430 435 440 445
 Thr Pro Gly Lys

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ile Lys Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Thr Glu Ala Ser Asn Leu Gln Ala Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Ile Ala Thr
 85

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Tyr Tyr Cys Gln Gln Tyr Gln Ser Leu Pro Tyr Thr Phe Gly Gln Gly
 1 5 10 15
 Thr Lys Leu Gln Ile Thr Arg
 20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser	Leu	Arg	Leu	Ser	Cys	Ser	Ser	Ser	Gly	Phe	Ile	Phe	Ser	Ser	Tyr
			20					25					30		
Ala	Met	Tyr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Ile	Ile	Trp	Asp	Asp	Gly	Ser	Asp	Gln	His	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Phe
65					70					75					80
Leu	Gln	Met	Asp	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Gly	Val	Tyr	Phe	Cys
				85					90					95	
Ala	Arg	Asp	Gly	Gly	His	Gly	Phe	Cys	Ser	Ser	Ala	Ser	Cys	Phe	Gly
			100					105					110		
Pro	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Pro	Val	Thr	Val	Ser	Ser		
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gln 1	Val	Gln	Leu 5	Val	Glu	Ser	Gly	Gly	Gly 10	Val	Val	Gln	Pro	Gly 15	Arg
Ser	Leu	Arg	Leu 20	Ser	Cys	Ser	Ser	Ser	Gly	Tyr	Thr	Phe	Thr 30	Arg	Tyr
Thr	Met	His 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45	Glu	Trp	Val
Ala	Tyr 50	Ile	Asn	Pro	Ser	Arg 55	Gly	Tyr	Thr	Asn	Tyr 60	Asn	Gln	Lys	Phe
Lys 65	Asp	Arg	Phe	Thr	Ile 70	Ser	Arg	Asp	Asn	Ser 75	Lys	Asn	Thr	Leu	Phe 80
Leu	Gln	Met	Asp	Ser 85	Leu	Arg	Pro	Glu	Asp 90	Thr	Gly	Val	Tyr	Phe 95	Cys
Ala	Arg	Tyr	Tyr 100	Asp	Asp	His	Tyr	Cys 105	Leu	Asp	Tyr	Trp	Gly 110	Gln	Gly

Thr Thr Leu Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	1	5	10	15
Ser	Leu	Arg	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	20	25	30	
Thr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	35	40	45	
Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Val	50	55	60	
Lys	Asp	Arg	Phe	Thr	Ile	Ser	Thr	Asp	Lys	Ser	Lys	Ser	Thr	Ala	Phe	65	70	75	80
Leu	Gln	Met	Asp	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	100	105	110	
Thr	Thr	Leu	Thr	Val	Ser	Ser										115			

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30
 Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Val
 50 55 60
 Lys Asp Arg Phe Thr Ile Ser Thr Asp Lys Ser Lys Ser Thr Ala Phe
 65 70 75 80
 Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
 85 90 95
 Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Thr Leu Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30
 Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Val
 50 55 60
 Lys Asp Arg Phe Thr Ile Ser Thr Asp Lys Ser Lys Asn Thr Ala Phe
 65 70 75 80
 Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
 85 90 95
 Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	1	5	10	15
Ser	Leu	Arg	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	20	25	30	
Thr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	35	40	45	
Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Val	50	55	60	
Lys	Asp	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Ala	Phe	65	70	75	80
Leu	Gln	Met	Asp	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Gly	Val	Tyr	Phe	Cys	85	90	95	
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	100	105	110	
Thr	Thr	Leu	Thr	Val	Ser	Ser										115			

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30
 Thr Met His Trp Val Arg Gln Ala Pro Cys Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Val
 50 55 60
 Lys Asp Arg Phe Thr Ile Ser Thr Asp Lys Ser Lys Asn Thr Leu Phe
 65 70 75 80
 Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
 85 90 95
 Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Thr Leu Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30
 Thr Met His Trp Val Arg Gln Ala Pro Cys Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Val
 50 55 60
 Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
 65 70 75 80
 Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
 85 90 95
 Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	1	5	10	15
Ser	Leu	Arg	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	20	25	30	
Thr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Cys	Lys	Gly	Leu	Glu	Trp	Val	35	40	45	
Ala	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Val	50	55	60	
Lys	Asp	Arg	Phe	Thr	Ile	Ser	Thr	Asp	Lys	Ser	Lys	Ser	Thr	Ala	Phe	65	70	75	80
Leu	Gln	Met	Asp	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Gly	Val	Tyr	Phe	Cys	85	90		
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	100	105	110	
Thr	Thr	Leu	Thr	Val	Ser	Ser										115			

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

Ser	Leu	Arg	Leu 20	Ser	Cys	Ser	Ala	Ser 25	Gly	Tyr	Thr	Phe	Thr 30	Arg	Tyr
Thr	Met	His 35	Trp	Val	Arg	Gln	Ala 40	Pro	Cys	Lys	Gly	Leu 45	Glu	Trp	Ile
Gly	Tyr 50	Ile	Asn	Pro	Ser	Arg 55	Gly	Tyr	Thr	Asn	Tyr 60	Asn	Gln	Lys	Val
Lys 65	Asp	Arg	Phe	Thr	Ile 70	Ser	Thr	Asp	Lys	Ser 75	Lys	Ser	Thr	Ala	Phe 80
Leu	Gln	Met	Asp	Ser 85	Leu	Arg	Pro	Glu	Asp 90	Thr	Ala	Val	Tyr	Tyr 95	Cys
Ala	Arg	Tyr	Tyr 100	Asp	Asp	His	Tyr	Cys 105	Leu	Asp	Tyr	Trp	Gly 110	Gln	Gly
Thr	Thr	Leu 115	Thr	Val	Ser	Ser									

(2) INFORMATION FOR SEQ ID NO:20:

(i). SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gln 1	Val	Gln	Leu	Val 5	Glu	Ser	Gly	Gly	Gly 10	Val	Val	Gln	Pro	Gly 15	Arg
Ser	Leu	Arg	Leu 20	Ser	Cys	Ser	Ala	Ser 25	Gly	Tyr	Thr	Phe	Thr 30	Arg	Tyr
Thr	Met	His 35	Trp	Val	Arg	Gln	Ala 40	Pro	Cys	Lys	Gly	Leu 45	Glu	Trp	Ile
Gly	Tyr 50	Ile	Asn	Pro	Ser	Arg 55	Gly	Tyr	Thr	Asn	Tyr 60	Asn	Gln	Lys	Val
Lys 65	Asp	Arg	Phe	Thr	Ile 70	Ser	Thr	Asp	Lys	Ser 75	Lys	Ser	Thr	Ala	Phe 80
Leu	Gln	Met	Asp	Ser 85	Leu	Arg	Pro	Glu	Asp 90	Thr	Ala	Val	Tyr	Tyr 95	Cys
Ala	Arg	Tyr	Tyr 100	Asp	Asp	His	Tyr	Cys 105	Leu	Asp	Tyr	Trp	Gly 110	Gln	Gly

Thr Thr Leu Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	1	5	10	15
Ser	Leu	Arg	Leu	Ser	Cys	Ser	Ser	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	20	25	30	
Thr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Cys	Lys	Gly	Leu	Glu	Trp	Ile	35	40	45	
Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Val	50	55	60	
Lys	Asp	Arg	Phe	Thr	Ile	Ser	Thr	Asp	Lys	Ser	Lys	Ser	Thr	Ala	Phe	65	70	75	80
Leu	Gln	Met	Asp	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	100	105	110	
Thr	Thr	Leu	Thr	Val	Ser	Ser										115			

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30
 Thr Met His Trp Val Arg Gln Ala Pro Cys Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Val
 50 55 60
 Lys Asp Arg Phe Thr Ile Ser Thr Asp Lys Ser Lys Ser Thr Ala Phe
 65 70 75 80
 Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
 85 90 95
 Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Thr Leu Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30
 Thr Met His Trp Val Arg Gln Ala Pro Cys Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Val
 50 55 60
 Lys Asp Arg Phe Thr Ile Ser Thr Asp Lys Ser Lys Ser Thr Ala Phe
 65 70 75 80
 Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
 85 90 95
 Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	1	5	10	15
Ser	Leu	Arg	Leu	Ser	Cys	Ser	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	20	25	30	
Thr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Cys	Lys	Gly	Leu	Glu	Trp	Ile	35	40	45	
Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Val	50	55	60	
Lys	Asp	Arg	Phe	Thr	Ile	Ser	Thr	Asp	Lys	Ser	Lys	Ser	Thr	Ala	Phe	65	70	75	80
Leu	Gln	Met	Asp	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Gly	Val	Tyr	Phe	Cys	85	90	95	
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	100	105	110	
Thr	Thr	Leu	Thr	Val	Ser	Ser										115			

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30
 Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
 65 70 75 80
 Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr
 85 90 95
 Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg
 100 105

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gln Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30
 Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 35 40 45
 Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
 65 70 75 80
 Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr
 85 90 95
 Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg
 100 105

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Gln	Ile	Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5				10						15		
Asp	Arg	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	
			20					25					30			
Asn	Trp	Tyr	Gln	Gln	Thr	Pro	Gly	Lys	Ala	Pro	Lys	Arg	Trp	Ile	Tyr	
		35					40					45				
Asp	Thr	Ser	Lys	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	
	50					55					60					
Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	
65				70						75					80	
Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ser	Asn	Pro	Phe	Thr	
			85						90					95		
Phe	Gly	Gln	Gly	Thr	Lys	Leu	Gln	Ile	Thr	Arg						
		100						105								

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5				10						15		
Asp	Arg	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	
			20					25					30			
Asn	Trp	Tyr	Gln	Gln	Thr	Pro	Gly	Lys	Ala	Pro	Lys	Arg	Trp	Ile	Tyr	
		35					40					45				

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg
100 105